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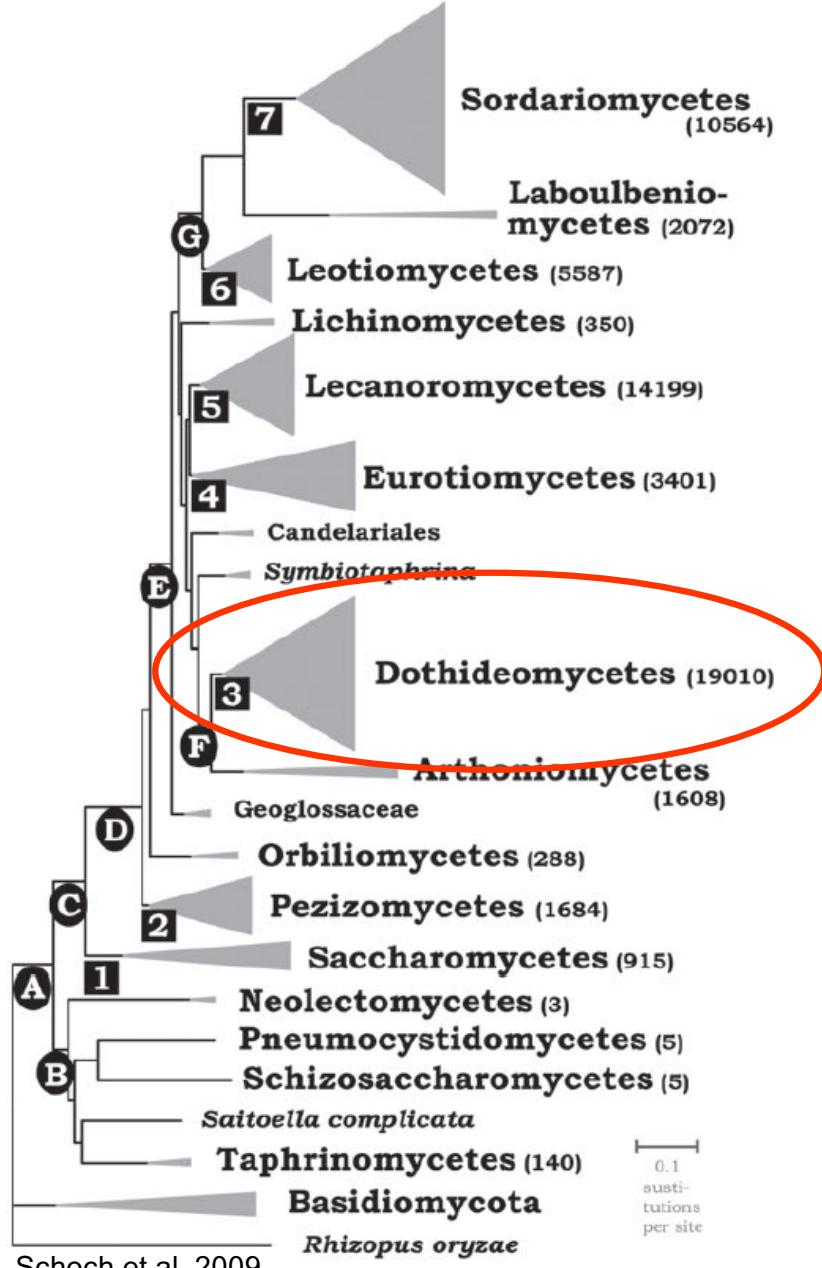


Evolutionary Genomics of Plant-Pathogenic Ascomycetes

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Dothideomycetes



- Largest and most diverse class of Ascomycetes
- Many plant pathogens:
 - *Cochliobolus*
 - *Setosphaeria/Exserohilum*
 - *Pyrenophora*
 - *Stagonospora*
 - *Leptosphaeria*
 - *Alternaria*
 - *Mycosphaerella/Zymoseptoria/Septoria*
 - *Dothistroma*
 - *Cladosporium*

Dothideomycetes

- Characteristics:
 - Ascolocular development
 - Bitunicate asci
 - Darkly pigmented



Pyrenophora phaeocomes

Background

- Evolutionary genomics of microbes:
 - Species recognition
 - Microbial adaptation
 - Molecular evolution
 - Signatures of positive selection
 - Antimicrobial resistance

Current Research Interests

- Associating genetic/genomic variation with relevant phenotypes in plant-pathogenic fungi:
 - Biosystematics, diagnostics
 - Pathogenicity, virulence
 - Speciation, host shifts
 - Secondary metabolites, fungicide resistance
 - Molecular evolution, selection

Alternaria

- Pathogen of wide range of hosts
- Pre- and post-harvest
- Leaf blotch/spot, fruit spot, early blight, black rot, sooty mold, black point, kernel smudge, etc.



E. McKenzie



UMN Extension



UMN Extension



Canadian Grain Commission

Alternaria

- Produces mycotoxins:
 - Altertoxin, alternariol/monomethyl ether, tenuazonic acid
 - Strong potential for regulation
- Problem for Phytosanitary Certification
- APHIS US Regulated Plant Pest = 6 species and *Alternaria sp.*

Taxonomy and Diagnostics

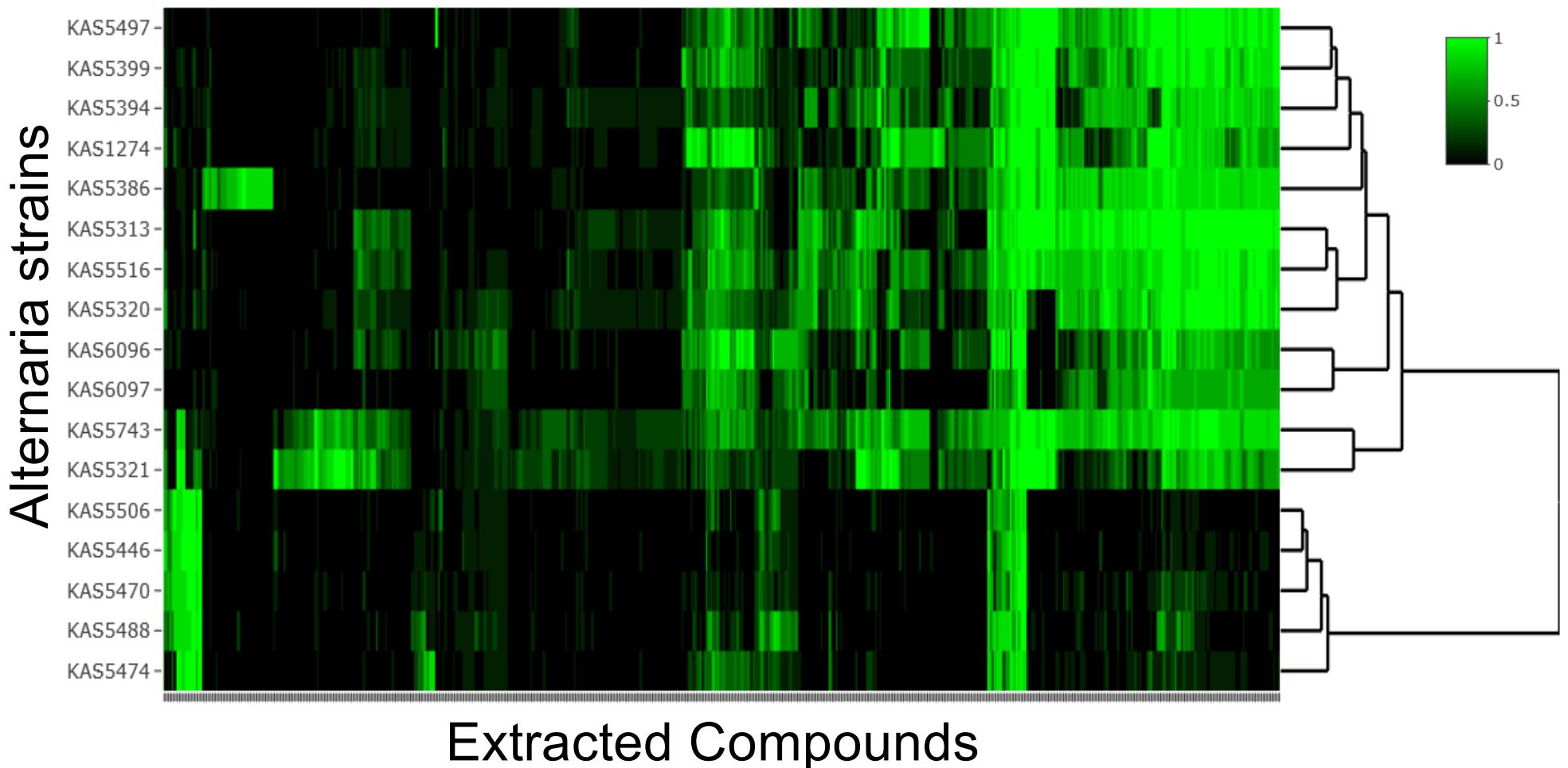


Section Alternaria



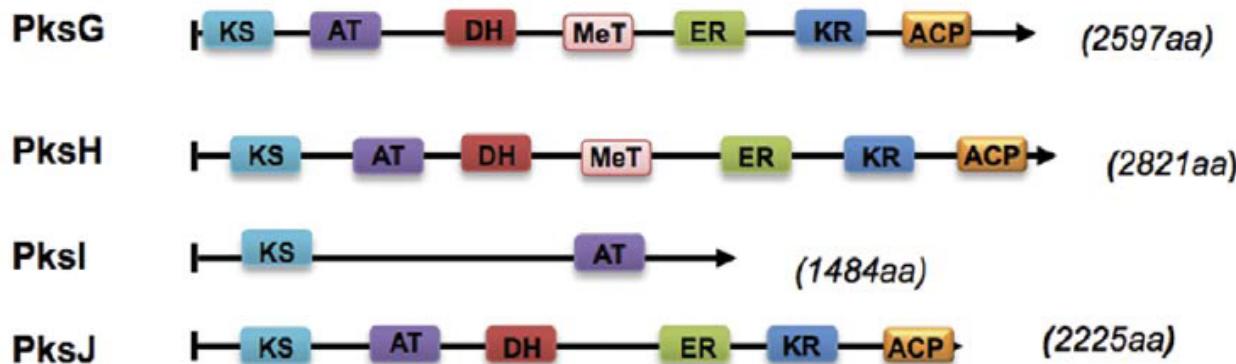
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Mycotoxin Production



Mycotoxin Prediction

- Is production strain- or species-specific?
- Conditionally dispensable chromosomes?
- Methods to detect gene clusters?



Examples of polyketide synthases in *A. alternata*
(Saha et al 2012)

Northern Corn Leaf Blight

- *Exserohilum turcicum* (*Setosphaeria turcica*)
- Greatest yield loss of any corn disease



L. Ramos-Romero



Jayasiri et al 2015

Canada

CCIFD
IEEMSI
GUISCP
RCCCRP

Northern Corn Leaf Blight

| Pathogen Race | Resistance Gene in Corn | | | | |
|---------------|-------------------------|------------|------------|-------------|-------------|
| | <i>Ht1</i> | <i>Ht2</i> | <i>Ht3</i> | <i>Htm1</i> | <i>Htn1</i> |
| 0 | - | - | - | - | - |
| 1 | + | - | - | - | - |
| 12 | + | + | - | - | - |
| 13M | + | - | + | + | - |
| 13MN | + | - | + | + | + |
| 123MN | + | + | + | + | + |

“+” denotes host susceptibility to infection, “-” denotes resistance



Northern Corn Leaf Blight

- What genetic/genomics differences define the various NCLB races?
 - 11.7K genes - 77% with no polymorphisms
- Molecular assay for race determination?
- Mechanisms of pathogenicity?
- Hyper-virulent races?



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